RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH
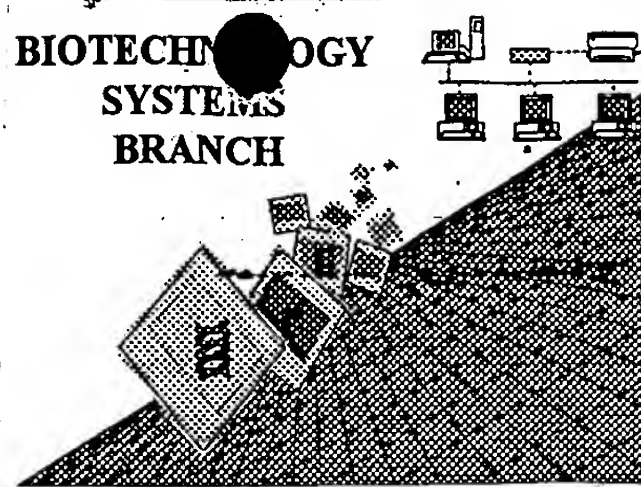
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/306,333_

Source: _1655_

Date Processed by STIC: _11/16/2000_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

1655

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/306,333*

DATE: 11/25/2000
TIME: 01:06:57

INPUT SET: S3614 **RECEIVED**

```
  1                                      SEQUENCE LISTING
  2
  3    (1)    General Information:
  4        (i) APPLICANT: Vijg, Jan
  5       (ii) TITLE OF INVENTION: BRCA1 And hMLH1 Gene Primer Sequences And
  6                                Method For Testing
  7      (iii) NUMBER OF SEQUENCES: 122
  8       (iv) CORRESPONDENCE ADDRESS:
  9            (A) ADDRESSEE: Rines & Rines
 10            (B) STREET: 81 North State Street
 11            (C) CITY: Concord
 12            (D) STATE: NH
 13            (E) COUNTRY: USA
 14            (F) ZIP: 03301
 15        (v) COMPUTER READABLE FORM:
 16            (A) MEDIUM TYPE: Diskette, 3.50 inch
 17            (B) COMPUTER: IBM PC
 18            (C) OPERATING SYSTEM: MS-DOS
 19            (D) SOFTWARE: Microsoft Wordpad
 20       (vi) CURRENT APPLICATION DATA:
 21            (A) APPLICATION NUMBER: US/09/306,333
 22            (B) FILING DATE: 06-May-1999
-->23            (C) CLASSIFICATION: <Unknown>
 24      (vii) PRIOR APPLICATION DATA:
 25     (viii) ATTORNEY/AGENT INFORMATION:
 26            (A) NAME: Rines, Robert H.
 27            (B) REGISTRATION NUMBER: 15,932
 28       (ix) TELECOMMUNICATION INFORMATION:
 29            (A) TELEPHONE: (603) 228-0121
 30            (B) TELEFAX: (603) 228-0210
```

OK → delete, if no information given

ERRORED SEQUENCES FOLLOW:

```
355    (2) INFORMATION FOR SEQ ID NO:19:
356        (i) SEQUENCE CHARACTERISTICS:
357            (A) LENGTH: 20 base pairs
358            (B) TYPE: nucleic acid
359            (C) STRANDEDNESS: double stranded
360            (D) TOPOLOGY: linear
361       (ii) MOLECULE TYPE: genomic DNA
362      (iii) HYPOTHETICAL: no
363       (iv) ANTI-SENSE: no
```

next page

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364          (vi) ORIGINAL SOURCE:
365               (A) ORGANISM: human
366         (vii) IMMEDIATE SOURCE:
367               (A) LIBRARY: genomic
368        (viii) POSITION IN GENOME:
369               (A) CHROMOSOME/SEGMENT: 3
370          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:
-->  371      CTTGCTCCTT CATGTTCTTG                                    18  20
372
```

```
605     (2) INFORMATION FOR SEQ ID NO:34:
606          (i) SEQUENCE CHARACTERISTICS:          37 shown
-->  607          (A) LENGTH: 18 base pairs
608               (B) TYPE: nucleic acid
609               (C) STRANDEDNESS: double stranded
610               (D) TOPOLOGY: linear
611         (ii) MOLECULE TYPE: genomic DNA
612        (iii) HYPOTHETICAL: no
613         (iv) ANTI-SENSE: no
614         (vi) ORIGINAL SOURCE:
615               (A) ORGANISM: human
616        (vii) IMMEDIATE SOURCE:
617               (A) LIBRARY: genomic
618       (viii) POSITION IN GENOME:
619               (A) CHROMOSOME/SEGMENT: 17
620         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:
621      GAGAAAGAAT GAATTGGAGT TGGATTTTCG TTCTCAC                   37
622
```

```
2027    (2) INFORMATION FOR SEQ ID NO:113:
2028         (i) SEQUENCE CHARACTERISTICS:          18 shown
-->  2029          (A) LENGTH: 19 base pairs
2030              (B) TYPE: nucleic acid
2031              (C) STRANDEDNESS: double stranded
2032              (D) TOPOLOGY: linear
2033        (ii) MOLECULE TYPE: genomic DNA
2034       (iii) HYPOTHETICAL: no
2035        (iv) ANTI-SENSE: no
2036        (vi) ORIGINAL SOURCE:
2037              (A) ORGANISM: human
2038       (vii) IMMEDIATE SOURCE:
2039              (A) LIBRARY: genomic
2040      (viii) POSITION IN GENOME:
2041              (A) CHROMOSOME/SEGMENT: 17
2042        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:      18  19
-->  2043     ATTCCCCTGT CCCTCTCT
2044
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/09/306,333*

INPUT SET: S36143.raw

Line	Error	Original Text
23	Wrong Classification	(C) CLASSIFICATION: <Unknown>
371	# of Sequences for line conflicts w/ running total	CTTGCTCCTT CATGTTCTTG
607	Entered (18) and Calc. Seq. Length (37) differ	(A) LENGTH: 18 base pairs
2029	Entered (19) and Calc. Seq. Length (18) differ	(A) LENGTH: 19 base pairs
2043	# of Sequences for line conflicts w/ running total	ATTCCCCTGT CCCTCTCT